

SEQUENCE LISTING

attachment # 7



<10> Sukhapinda, Kitisri  
 Hasler, James M  
 Petell, James K  
 Strickland, James A  
 Folkerts, Otto

<110> ANTIBODY-MEDIATED DOWN-REGULATION OF PLANT PROTEINS

<130> 50447

<140> US 09/358,321

<141> 1999-07-21

<150> US 60/093,587

<151> 1998-07-21

<160> 56

<170> PatentIn Ver. 2.0

<210> 1

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:5' primer

<220>

<221> unsure

<222> (12)

<223> n can be a,t,g, or c in this degenerate primer

<400> 1

gargaraaym gncaygg

17

<210> 2

<211> 18

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<220>

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<220>

<221> unsure

<222> (7)

<223> n can be a,t,g, or c in this degenerate primer

<400> 2

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18

<210> 3

<211> 276

<212> DNA

<213> Zea mays

<220>  
 <221> CDS  
 <222> (1)..(276)

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 Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr  
 1 5 10 15  
 ggg agg gtg gat atg agg cag att gag aag aca att cag tat ctt att 96  
 Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile  
 20 25 30  
 ggc tct gga atg gat cct agg act gag aat aat cct tat ctt ggt ttc 144  
 Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe  
 35 40 45  
 atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac ggg aac 192  
 Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn  
 50 55 60  
 act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca caa atc 240  
 Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile  
 65 70 75 80  
 tgc ggc atc atc gcc tca gat gag aag cga cat gaa 276  
 Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu  
 85 90

<210> 4  
 <211> 92  
 <212> PRT  
 <213> Zea mays

<400> 4  
 Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr  
 1 5 10 15  
 Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile  
 20 25 30  
 Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe  
 35 40 45  
 Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn  
 50 55 60  
 Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile  
 65 70 75 80  
 Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu  
 85 90

<210> 5  
 <211> 1621  
 <212> DNA  
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Leu Thr Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr	
155 160 165 170	
ctt att ggc tct gga atg gat cct agg act gag aat aat cct tat ctt	796
Leu Ile Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu	
175 180 185	
ggg ttc atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac	844
Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His	
190 195 200	
ggg aac act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca	892
Gly Asn Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala	
205 210 215	
caa atc tgc ggc atc atc gcc tca gat gag aag cga cat gaa act gcg	940
Gln Ile Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala	
220 225 230	
tac acc aag atc gtg gag aag ctg ttt gag atc gac cct gat ggt acc	988
Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr	
235 240 245 250	
gtg gtc gct ctg gct gac atg atg agg aag aag atc tca atg cct gcc	1036
Val Val Ala Leu Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala	
255 260 265	
cac ctg atg ttt gac ggg cag gac gac aag ctg ttc gag cac ttc tcc	1084
His Leu Met Phe Asp Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser	
270 275 280	
atg gtc gcg cag agg ctt ggc gtt tac acc gcc agg gac tac gcc gac	1132
Met Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp	
285 290 295	
atc ctc gag ttc ctc gtc gac agg tgg aag gtg gcg agc ctg act ggt	1180
Ile Leu Glu Phe Leu Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly	
300 305 310	
ctg tcg ggt gaa ggg aac aag gcg cag gac tac ctt tgc acc ctt gct	1228
Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala	
315 320 325 330	
tca aga atc agg agg ctg gag gag agg gcc cag agc aga gcc aag aaa	1276
Ser Arg Ile Arg Arg Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys	
335 340 345	
gcc ggc acg ctg cct ttc agc tgg gta tac ggt agg gac gtc caa ctg	1324
Ala Gly Thr Leu Pro Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu	
350 355 360	
tgagatcgga aacctgctgc ggactgotta gacaagacct gctgtgtctg cgttacatag	1384
gtctccaggt tttgatcaaa tgggtcccggtg tcgtcttata gagcgatagg agaacgtggt	1444
gggtctgtggt gtagctttgt ttttatcttg tatttttctg ctttgatgta caacctgtgg	1504
ccgcatgaac tggggcgtgg agatgggagc gaccatgccg tactttgtct gtcgctggcg	1564
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Ala	Ala	Arg	Arg	Arg	Arg	Arg	Ser	Ser	Gly	Arg	Phe	Val	Ala	Val	Ala	
-15					-10					-5				-1	1	
Ser	Met	Thr	Ser	Ala	Val	Ser	Thr	Lys	Val	Glu	Asn	Lys	Lys	Pro	Phe	
			5					10					15			
Ala	Pro	Pro	Arg	Glu	Val	His	Val	Gln	Val	Thr	His	Ser	Met	Pro	Pro	
		20					25					30				
His	Lys	Ile	Glu	Ile	Phe	Lys	Ser	Leu	Asp	Asp	Trp	Ala	Arg	Asp	Asn	
	35					40					45					
Ile	Leu	Thr	His	Leu	Lys	Pro	Val	Glu	Lys	Cys	Trp	Gln	Pro	Gln	Asp	
	50				55					60					65	
Phe	Leu	Pro	Asp	Pro	Ala	Ser	Glu	Gly	Phe	His	Asp	Glu	Val	Lys	Glu	
				70					75					80		
Leu	Arg	Glu	Arg	Ala	Lys	Glu	Ile	Pro	Asp	Asp	Tyr	Phe	Val	Cys	Leu	
			85					90					95			
Val	Gly	Asp	Met	Ile	Thr	Glu	Glu	Ala	Leu	Pro	Thr	Tyr	Gln	Thr	Met	
		100					105						110			
Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg	Asp	Glu	Thr	Gly	Ala	Ser	Pro	Thr	
	115					120					125					
Ala	Trp	Ala	Val	Trp	Thr	Arg	Ala	Trp	Thr	Ala	Glu	Glu	Asn	Arg	His	
130					135					140					145	
Gly	Asp	Leu	Leu	Asn	Lys	Tyr	Met	Tyr	Leu	Thr	Gly	Arg	Val	Asp	Met	
				150					155					160		
Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser	Gly	Met	Asp	
			165					170					175			
Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe	Ile	Tyr	Thr	Ser	Phe	
		180					185					190				
Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala	Arg	His	Ala	
	195					200					205					
Lys	Asp	Phe	Gly	Asp	Leu	Lys	Leu	Ala	Gln	Ile	Cys	Gly	Ile	Ile	Ala	
210					215					220					225	
Ser	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile	Val	Glu	Lys	
				230					235					240		
Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly	Thr	Val	Val	Ala	Leu	Ala	Asp	Met	
			245					250					255			

Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp Gly Gln  
260 265 270

Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg Leu Gly  
275 280 285

Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Asp  
290 295 300 305

Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys  
310 315 320

Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg Leu Glu  
325 330 335

Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro Phe Ser  
340 345 350

Trp Val Tyr Gly Arg Asp Val Gln Leu  
355 360

<210> 7  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 7  
atggctagcc tccgcctcaa cgacgtcgcg 30

<210> 8  
<211> 36  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:primer

<400> 8  
aaagctagct catcacagtt ggacgtccct accgta 36

<210> 9  
<211> 30  
<212> DNA  
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<220>  
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<400> 9  
accatggcta gcatgacgtc cgccgtctcc 30

<210> 10  
<211> 30

<212> DNA  
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<220>  
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<400> 10  
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<210> 11  
 <211> 1107  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (4)..(1092)

<400> 11  
 acc atg gct acg atg acg tcc gcc gtc tcc acc aag gtc gag aat aag 48  
 Met Ala Thr Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys  
 1 5 10 15

aag cca ttt gct cct cca agg gag gta cat gtc cag gtt aca cat tca 96  
 Lys Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser  
 20 25 30

atg cca cct cac aag att gaa att ttc aag tcg ctt gat gat tgg gct 144  
 Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala  
 35 40 45

aga gat aat atc ttg acg cat ctc aag cca gtc gag aag tgt tgg cag 192  
 Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln  
 50 55 60

cca cag gat ttc ctc ccg gac cca gca tct gaa gga ttt cat gat gaa 240  
 Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu  
 65 70 75

gtt aag gag ctc aga gaa cgt gcc aag gaa atc cct gat gat tat ttt 288  
 Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe  
 80 85 90 95

gtt tgt ttg gtg gga gac atg att acc gag gaa gct cta cca aca tac 336  
 Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr  
 100 105 110

cag act atg ctt aac acc ctc gac ggt gtc aga gat gag aca ggt gca 384  
 Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala  
 115 120 125

agc ccc act gcc tgg gct gtt tgg acg agg gca tgg act gct gag gag 432  
 Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu  
 130 135 140

aac agg cat ggt gat ctg ctc aac aag tat atg tac ctc act ggg agg 480  
 Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg  
 145 150 155

gtg gat atg agg cag att gag aag aca att cag tat ctt att ggc tct 528

Val	Asp	Met	Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser	
160					165					170					175	
gga	atg	gat	cct	agg	act	gag	aat	aat	cct	tat	ctt	ggt	ttc	atc	tac	576
Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe	Ile	Tyr	
				180					185					190		
acc	tcc	ttc	caa	gag	cgg	gcg	acc	ttc	atc	tca	cac	ggg	aac	act	gct	624
Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala	
			195					200					205			
cgt	cac	gcc	aag	gac	ttt	ggc	gac	tta	aag	ctt	gca	caa	atc	tgc	ggc	672
Arg	His	Ala	Lys	Asp	Phe	Gly	Asp	Leu	Lys	Leu	Ala	Gln	Ile	Cys	Gly	
		210					215					220				
atc	atc	gcc	tca	gat	gag	aag	cga	cat	gaa	act	gcg	tac	acc	aag	atc	720
Ile	Ile	Ala	Ser	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile	
	225					230					235					
gtg	gag	aag	ctg	ttt	gag	atc	gac	cct	gat	ggg	acc	gtg	gtc	gct	ctg	768
Val	Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly	Thr	Val	Val	Ala	Leu	
240					245					250				255		
gct	gac	atg	atg	agg	aag	aag	atc	tca	atg	cct	gcc	cac	ctg	atg	ttt	816
Ala	Asp	Met	Met	Arg	Lys	Lys	Ile	Ser	Met	Pro	Ala	His	Leu	Met	Phe	
				260					265					270		
gac	ggg	cag	gac	gac	aag	ctg	ttc	gag	cac	ttc	tcc	atg	gtc	gcg	cag	864
Asp	Gly	Gln	Asp	Asp	Lys	Leu	Phe	Glu	His	Phe	Ser	Met	Val	Ala	Gln	
			275					280					285			
agg	ctt	ggc	gtt	tac	acc	gcc	agg	gac	tac	gcc	gac	atc	ctc	gag	ttc	912
Arg	Leu	Gly	Val	Tyr	Thr	Ala	Arg	Asp	Tyr	Ala	Asp	Ile	Leu	Glu	Phe	
	290						295					300				
ctc	gtc	gac	agg	tgg	aag	gtg	gcg	agc	ctg	act	ggg	ctg	tcg	ggg	gaa	960
Leu	Val	Asp	Arg	Trp	Lys	Val	Ala	Ser	Leu	Thr	Gly	Leu	Ser	Gly	Glu	
	305					310					315					
ggg	aac	aag	gcg	cag	gac	tac	ctt	tgc	acc	ctt	gct	tca	aga	atc	agg	1008
Gly	Asn	Lys	Ala	Gln	Asp	Tyr	Leu	Cys	Thr	Leu	Ala	Ser	Arg	Ile	Arg	
320					325					330				335		
agg	ctg	gag	gag	agg	gcc	cag	agc	aga	gcc	aag	aaa	gcc	ggc	acg	ctg	1056
Arg	Leu	Glu	Glu	Arg	Ala	Gln	Ser	Arg	Ala	Lys	Lys	Ala	Gly	Thr	Leu	
				340					345					350		
cct	ttc	agc	tgg	gta	tac	ggg	agg	gac	gtc	caa	ctg	tgagctagca	tcac			1107
Pro	Phe	Ser	Trp	Val	Tyr	Gly	Arg	Asp	Val	Gln	Leu					
			355					360								

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 <212> PRT  
 <213> Zea mays

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 Met Ala Thr Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys Lys  
 1 5 10 15



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Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg  
                     35                                    40                                    45

Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro  
                     50                                    55                                    60

Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu Val  
                     65                                    70                                    75                                    80

Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val  
                                     85                                    90                                    95

Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln  
                                     100                                    105                                    110

Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser  
                     115                                    120                                    125

Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn  
                     130                                    135                                    140

Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val  
                     145                                    150                                    155                                    160

Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly  
                                     165                                    170                                    175

Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr  
                     180                                    185                                    190

Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg  
                     195                                    200                                    205

His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Ile  
                     210                                    215                                    220

Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val  
                     225                                    230                                    235                                    240

Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu Ala  
                                     245                                    250                                    255

Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp  
                     260                                    265                                    270

Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg  
                     275                                    280                                    285

Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu  
                     290                                    295                                    300

Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly  
                     305                                    310                                    315                                    320

Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg  
                     325                                    330                                    335

Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro

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340
345
350
Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu
355 360

<210> 13
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<212> PRT
<213> Zea mays

<400> 13
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1 5

<210> 14
<211> 10
<212> PRT
<213> Zea mays

<220>
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<222> (8)
<223> unknown

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1 5 10

<210> 15
<211> 31
<212> PRT
<213> Zea mays

<400> 15
Met Ala Leu Arg Leu Asn Asp Val Ala Leu Cys Leu Ser Pro Pro Leu
1 5 10 15

Ala Ala Arg Arg Arg Arg Ser Ser Gly Arg Phe Val Ala Val
20 25 30

<210> 16
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 16
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<210> 17
<211> 36
<212> DNA
<213> Artificial Sequence

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<220>  
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 <210> 18  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:primer  
  
 <400> 18  
 tacgttacct gageggccgc gctgggctca agttttttgt ccaccg 46  
  
 <210> 19  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:primer  
  
 <400> 19  
 ttgctagct tactaacact cattcctggt gaagctct 38  
  
 <210> 20  
 <211> 102  
 <212> DNA  
 <213> Artificial Sequence  
  
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 cattctgect ttgcggcggt tgtgatgacc ccaaaccac tc 102  
  
 <210> 21  
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 <212> DNA  
 <213> mouse  
  
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 <221> unsure  
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 <223> not known  
  
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 <222> (26)  
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<222> (37) .. (693)
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<400> 21

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tgc Cys	aga Arg	tct Ser 25	agt Ser	cag Gln	agc Ser	ctt Leu	tta Leu 30	cac His	agt Ser	aat Asn	gga Gly	atc Ile 35	acc Thr	tat Tyr	tta Leu	150
cat His	tgg Trp 40	tac Tyr	ctg Leu	cag Gln	aag Lys	cca Pro 45	ggc Gly	cag Gln	tct Ser	cca Pro	aag Lys 50	ctc Leu	ctg Leu	atc Ile	tac Tyr	198
aaa Lys 55	gtt Val	tcc Ser	aac Asn	cga Arg	ttt Phe 60	tct Ser	ggg Gly	gtc Val	cca Pro	gac Asp 65	agg Arg	ttc Phe	agt Ser	ggc Gly 70	agt Ser 70	246
gga Gly	tca Ser	ggg Gly	aca Thr 75	gat Asp	ttc Phe	aca Thr	ctc Leu	aag Lys	atc Ile 80	aac Asn	aga Arg	gtg Val	gag Glu	gct Ala 85	gag Glu	294
gat Asp	ctg Leu	gga Gly	gtt Val 90	tat Tyr	ttc Phe	tgc Cys	tct Ser	caa Gln 95	agt Ser	aca Thr	cat His	gtt Val 100	cct Pro	tac Tyr	acg Thr	342
ttc Phe	gga Gly 105	ggg Gly	ggg Gly	acc Thr	aag Lys	ctg Leu	gaa Glu 110	ata Ile	aaa Lys	cgg Arg	gct Ala	gat Asp 115	gct Ala	gca Ala	cca Pro	390
act Thr 120	gta Val	tcc Ser	atc Ile	ttc Phe	cca Pro	cca Pro 125	tcc Ser	agt Ser	gag Glu	cag Gln	tta Leu 130	aca Thr	tct Ser	gga Gly	ggt Gly	438
gcc Ala 135	tca Ser	gtc Val	gtg Val	tgc Cys	ttc Phe 140	ttg Leu	aac Asn	aac Asn	ttc Phe	tac Tyr 145	ccc Pro	aaa Lys	gac Asp	atc Ile	aat Asn 150	486
gtc Val	aag Lys	tgg Trp	aag Lys 155	att Ile	gat Asp	ggc Gly	agt Ser	gaa Glu	cga Arg 160	caa Gln	aat Asn	ggc Gly	gtc Val 165	ctg Leu	aac Asn	534
agt Ser	tgg Trp	act Thr	gat Asp 170	cag Gln	gac Asp	acc Thr	aaa Lys	gac Asp 175	agc Ser	acc Thr	tac Tyr	agc Ser	atg Met 180	agc Ser	agc Ser	582
acc Thr	ctc Leu 185	acg Thr	ttg Leu	acc Thr	aag Lys	gac Asp	gag Glu 190	tat Tyr	gaa Glu	cga Arg	cat His	aac Asn 195	agc Ser	tat Tyr	acc Thr	630

tgt gag gcc act cac aag aca tca act tca ccc att gtc aag agc ttc	678
Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe	
200 205 210	

aac agg aat gag tgt tagtaagcta gcacgcccga tgggtgggacg gtatgaataa	733
Asn Arg Asn Glu Cys	
215	

tccgg	738
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<210> 22  
 <211> 336  
 <212> DNA  
 <213> mouse

<220>  
 <221> CDS  
 <222> (1)..(336)

<400> 22	
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Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly	
1 5 10 15	

gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt	96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
20 25 30	

aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct	144
Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	

cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca	192
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50 55 60	

gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65 70 75 80	

aac aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt	288
Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser	
85 90 95	

aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa	336
Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
100 105 110	

<210> 23  
 <211> 108  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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gcgcattctg cctttgcggc ggttcaactg cagcagtctg gggctgag

108

<210> 24  
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<212> DNA  
<213> mouse

<220>  
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<222> (25)..(837)

<220>  
<221> mat\_peptide  
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<400> 24

ctgcagggta cggccatatt ggcc atg act atc ctt tgc tgg ctg gcc ctt	51
Met Thr Ile Leu Cys Trp Leu Ala Leu	
-15 -10	
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Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn	
-5 -1 1 5	
cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc	147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys	
10 15 20	
aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat	195
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His	
25 30 35	
tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa	243
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys	
40 45 50 55	
gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga	291
Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly	
60 65 70	
tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat	339
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp	
75 80 85	
ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc	387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe	
90 95 100	
gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc	435
Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly	
105 110 115	
aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag	483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln	
120 125 130 135	
cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc	531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser	
140 145 150	

tgc aag gct tgc ggc tac aca ttt act gac tat gaa ata cac tgg gtg	579
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val	
155 160 165	
agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct	627
Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro	
170 175 180	
gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata	675
Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile	
185 190 195	
gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc	723
Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser	
200 205 210 215	
ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag	771
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu	
220 225 230	
gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct	819
Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser	
235 240 245	
cat cat cat cat cat cat tagggcctct ctggccgatc ccccgaattt	867
His His His His His His	
250	
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<210> 25	
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<213> mouse	
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<221> CDS	
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Gln Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly	
1 5 10 15	
gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt	96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
20 25 30	
aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct	144
Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	
cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca	192
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50 55 60	
gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65 70 75 80	

agc	aga	gtg	gag	gct	gag	gat	ctg	gga	gtt	tat	ttc	tgc	tct	caa	agt	288
Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	
			85						90					95		

aca	cat	gtt	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aag	ctg	gaa	ata	aaa	336
Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	
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ggc																339
Gly																

<210> 26  
 <211> 64  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 26  
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 agtc 64

<210> 27  
 <211> 63  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 27  
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 aac 63

<210> 28  
 <211> 78  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 28  
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 tttatttcca gcttggtc 78

<210> 29  
 <211> 459  
 <212> DNA  
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<220>



<221> CDS  
 <222> (19)..(459)

<220>  
 <221> mat\_peptide  
 <222> (79)..(459)

<400> 29  
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                           Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu  
                           -20                          -15                          -10

gcg gcg gcg gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct 99  
 Ala Ala Ala Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser  
                           -5                          -1 1                          5

ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag 147  
 Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys  
                           10                          15                          20

gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg agg cag 195  
 Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln  
                           25                          30                          35

aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act 243  
 Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr  
                           40                          45                          50                          55

ggg ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act 291  
 Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr  
                           60                          65                          70

gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca 339  
 Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr  
                           75                          80                          85

tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg 387  
 Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp  
                           90                          95                          100

ggc caa ggg act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga 435  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly  
                           105                          110                          115

tct ggc tcc gaa tcc aaa ccc ggg 459  
 Ser Gly Ser Glu Ser Lys Pro Gly  
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<210> 30  
 <211> 438  
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<220>  
 <221> CDS  
 <222> (1)..(408)

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gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga gat caa	96			
Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln				
20 25 30				
gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt aat gga	144			
Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly				
35 40 45				
atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aag	192			
Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys				
50 55 60				
ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg	240			
Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg				
65 70 75 80				
ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc agc aga	288			
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg				
85 90 95				
gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat	336			
Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His				
100 105 110				
gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa gaa gaa	384			
Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Glu Glu				
115 120 125				
aaa ctc atc tca gaa gag gat ctg aattagtaag gggccgcctt gacctagtgc	438			
Lys Leu Ile Ser Glu Glu Asp Leu				
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gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag	96			
Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu				
-5 -1 1 5 10				
ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tcg ggc	144			
Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly				
15 20 25				

tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg	192
Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val	
30 35 40	
cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act	240
His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr	
45 50 55	
gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa	288
Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys	
60 65 70	
tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac	336
Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp	
75 80 85 90	
tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg	384
Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly	
95 100 105	
act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga tct ggc tcc	432
Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly Ser Gly Ser	
110 115 120	
gaa tcc aaa ccc ggg gat gtt gtg atg acc cca aac cca ctc tcc ctg	480
Glu Ser Lys Pro Gly Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu	
125 130 135	
cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag	528
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln	
140 145 150	
agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac ctg cag	576
Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln	
155 160 165 170	
aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga	624
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg	
175 180 185	
ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat	672
Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
190 195 200	
ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat	720
Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr	
205 210 215	
ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc	768
Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr	
220 225 230	
aag ctg gaa ata aaa gaa gaa aaa ctc atc tca gaa gag gat ctg	813
Lys Leu Glu Ile Lys Glu Glu Lys Leu Ile Ser Glu Glu Asp Leu	
235 240 245	
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<210> 32

<211> 269

<212> PRT  
 <213> mouse

<400> 32

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Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala Ala His
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          -1   1           5           10

Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr
          15           20           25

Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val His Gly
          30           35           40

Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr Ala Tyr
          45           50           55           60

Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys Ser Ser
          65           70           75

Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala
          80           85           90

Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly Thr Leu
          95           100          105

Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser
          110          115          120

Lys Pro Gly Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val
125          130          135          140

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
          145          150          155

Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
          160          165          170

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
          175          180          185

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
          190          195          200

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
205          210          215          220

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
          225          230          235

Glu Ile Lys Glu Glu Lys Leu Ile Ser Glu Glu Asp Leu
          240          245

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<210> 33  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:c-myc tag

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<210> 34  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:p67 leader

<400> 34  
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<210> 35  
 <211> 84  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 35  
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 gccgtcaacg ctgcggttgt gatg 84

<210> 36  
 <211> 70  
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<220>  
 <223> Description of Artificial Sequence:primer

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 cagcttggtc 70

<210> 37  
 <211> 74  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 37  
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 caactgcagc agtc 74

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<210> 38
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 38
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gtgaccagag tc 72

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<210> 39
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 39
aaaatttgcg gccgcctaata gatgatgatg atgatgagaa c 41

<210> 40
<211> 462
<212> DNA
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<220>
<221> CDS
<222> (19)..(462)

<220>
<221> mat_peptide
<222> (73)..(462)

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Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser
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act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc 99
Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu
-5 -1 1 5

tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct 147
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
10 15 20 25

agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac 195
Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr
30 35 40

ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc 243
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
45 50 55

aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg 291

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Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly		
	75					80				85							
gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	ccg	tac	acg	ttc	gga	ggg	387	
Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly		
	90				95				100					105			
ggg	acc	aag	ctg	gaa	ata	aaa	ggc	agc	acc	agc	ggc	agc	ggc	aag	ccg	435	
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro		
			110					115						120			
ggc	agc	ggc	gag	ggc	agc	acc	aag	ggc								462	
Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly									
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<211> 443																	
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<222> (1) .. (423)																	
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	1			5				10						15			
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Lys	Gly	His	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro		
			20					25					30				
ggg	gct	tca	gtg	acg	ctg	tcc	tgc	aag	gct	tcg	ggc	tac	aca	ttt	act	144	
Gly	Ala	Ser	Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr		
		35					40					45					
gac	tat	gaa	ata	cac	tgg	gtg	aag	cag	aca	cct	gtg	cat	ggc	ctg	gaa	192	
Asp	Tyr	Glu	Ile	His	Trp	Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Glu		
	50					55				60							
tgg	att	gga	gct	att	gat	cct	gaa	act	ggc	ggc	act	gcc	tac	aat	cag	240	
Trp	Ile	Gly	Ala	Ile	Asp	Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln		
	65				70				75					80			
aag	ttc	aag	gac	aag	gcc	ata	gtg	act	gta	gac	aaa	tcc	tcc	agc	aca	288	
Lys	Phe	Lys	Asp	Lys	Ala	Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr		
			85					90						95			
gcc	tac	atg	gag	ctc	cgc	agc	ctg	aca	tct	gaa	gac	tct	gcc	gtc	tat	336	
Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr		
			100					105					110				
tac	tat	aca	aga	tgg	ttt	gag	gac	tgg	ggc	caa	ggg	act	ctg	gtc	act	384	
Tyr	Tyr	Thr	Arg	Trp	Phe	Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr		
		115					120					125					

gtc tct gca atg cgg ggt tct cat cat cat cat cat cat ggggccgctt	433
Val Ser Ala Met Arg Gly Ser His His His His His His	
130 135 140	

gacctagtagc 443

<210> 42  
 <211> 851  
 <212> DNA  
 <213> mouse

<220>  
 <221> CDS  
 <222> (19)..(831)

<220>  
 <221> mat\_peptide  
 <222> (73)..(831)

<400> 42	
gcactagggtc aatctaga atg act atc ctt tgc tgg cta gcc ctt ctg tca	51
Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser	
-15 -10	
act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc	99
Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu	
-5 -1 1 5	
tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct	147
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser	
10 15 20 25	
agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac	195
Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr	
30 35 40	
ctg cag aag cca gcc cag tct cca aag ctc ctg atc tac aaa gtt tcc	243
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser	
45 50 55	
aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg	291
Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly	
60 65 70	
aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga	339
Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly	
75 80 85	
gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg	387
Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly	
90 95 100 105	
ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag ccg	435
Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro	
110 115 120	
ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag cag tct	483
Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln Gln Ser	
125 130 135	



```

ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag 531
Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys
      140                      145                      150

gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg aag cag 579
Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Lys Gln
      155                      160                      165

aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act 627
Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr
      170                      175                      180                      185

ggg ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act 675
Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr
      190                      195                      200

gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca 723
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr
      205                      210                      215

tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg 771
Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp
      220                      225                      230

ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct cat cat 819
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser His His
      235                      240                      245

cat cat cat cat gcggccgctt gacctagtgc 851
His His His His
      250

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<210> 43
<211> 867
<212> DNA
<213> mouse

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<220>
<221> CDS
<222> (31)..(843)

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<220>
<221> mat_peptide
<222> (85)..(843)

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<400> 43
aatttaaagc gatcccggtt accttctaga atg act atc ctt tgc tgg cta gcc 54
      Met Thr Ile Leu Cys Trp Leu Ala
                        -15

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ctt ctg tca act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca 102
Leu Leu Ser Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro
-10                      -5                      -1 1                      5

```

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aac cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 150
Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
      10                      15                      20

```

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tgc aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta 198

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Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu		
		25					30					35					
cat	tgg	tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aag	ctc	ctg	atc	tac	246	
His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr		
	40					45					50						
aaa	gtt	tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	294	
Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser		
	55				60					65					70		
gga	tca	ggg	aca	gat	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	gag	342	
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu		
				75					80					85			
gat	ctg	gga	gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	ccg	tac	acg	390	
Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr		
			90					95					100				
ttc	gga	ggg	ggg	acc	aag	ctg	gaa	ata	aaa	ggc	agc	acc	agc	ggc	agc	438	
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser		
		105					110					115					
ggc	aag	ccg	ggc	agc	ggc	gag	ggc	agc	acc	aag	ggc	cat	gtt	caa	ctg	486	
Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	His	Val	Gln	Leu		
	120					125					130						
cag	cag	tct	ggg	gct	gag	ctg	gtg	agg	cct	ggg	gct	tca	gtg	acg	ctg	534	
Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	Ser	Val	Thr	Leu		
	135				140					145					150		
tcc	tgc	aag	gct	tcg	ggc	tac	aca	ttt	act	gac	tat	gaa	ata	cac	tgg	582	
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Glu	Ile	His	Trp		
				155					160					165			
gtg	aag	cag	aca	cct	gtg	cat	ggc	ctg	gaa	tgg	att	gga	gct	att	gat	630	
Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Asp		
			170					175					180				
cct	gaa	act	ggt	ggt	act	gcc	tac	aat	cag	aag	ttc	aag	gac	aag	gcc	678	
Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala		
		185					190					195					
ata	gtg	act	gta	gac	aaa	tcc	tcc	agc	aca	gcc	tac	atg	gag	ctc	cgc	726	
Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg		
	200					205					210						
agc	ctg	aca	tct	gaa	gac	tct	gcc	gtc	tat	tac	tat	aca	aga	tgg	ttt	774	
Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Tyr	Thr	Arg	Trp	Phe		
	215				220					225					230		
gag	gac	tgg	ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	atg	cgg	ggc	822	
Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Met	Arg	Gly		
				235				240						245			
tct	cat	cat	cat	cat	cat	cat	cat	taggcggccg	ctgcagatct	gatc						867	
Ser	His	His	His	His	His	His											
			250														

<210> 44

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<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 44
tttaaaggcc atattggcca tgactatcct ttgctggct 39

<210> 45
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 45
tttaaaggcc atattggcca tggatgttgt gatgacccca aac 43

<210> 46
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 46
tttaaaggcc agagaggccc taatgatgat gatgatgatg agaacccccgc attg 54

<210> 47
<211> 882
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (25)..(837)

<220>
<221> mat_peptide
<222> (79)..(837)

<400> 47
ctgcagggta cggccatatt ggcc atg act atc ctt tgc tgg ctg gcc ctt 51
                               Met Thr Ile Leu Cys Trp Leu Ala Leu
                               -15                               -10

ctg tca act ctg act gcc gtc aac act gcg gtt gtg atg acc cca aac 99
Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn
      -5              -1   1              5

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
      10              15              20

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aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat	195
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His	
25 30 35	
tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa	243
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys	
40 45 50 55	
ggt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga	291
Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly	
60 65 70	
tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat	339
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp	
75 80 85	
ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc	387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe	
90 95 100	
gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc	435
Gly Gly Gly Thr Lys Leu Ile Lys Gly Ser Thr Ser Gly Ser Gly	
105 110 115	
aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag	483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln	
120 125 130 135	
cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc	531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser	
140 145 150	
tgc aag gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg	579
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val	
155 160 165	
agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct	627
Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro	
170 175 180	
gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata	675
Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile	
185 190 195	
gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc	723
Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser	
200 205 210 215	
ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag	771
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu	
220 225 230	
gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct	819
Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser	
235 240 245	
cat cat cat cat cat cat tagggcctct ctggccgata ccccgaaattt	867
His His His His His His	
250	
ccccgatcgt tcaaaa	882

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<220>
<221> CDS
<222> (25)..(786)
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ctgcagggta cggccatatt ggcc atg gat gtt gtg atg acc cca aac cca 51  
Met Asp Val Val Met Thr Pro Asn Pro  
1 5

ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga 99  
Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg  
10 15 20 25

tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg 147  
Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp  
30 35 40

tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aag	ctc	ctg	atc	tac	aaa	gtt	195
Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	
			45					50					55			

tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca 243  
Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser  
60 65 70

ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg 291  
Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu  
75 80 85

gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga 339  
Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly  
90 95 100 105

ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag 387  
Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys  
110 115 120

ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag cag 435  
Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln Gln  
125 130 135

tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc 483  
Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys  
140 145 150

aag gct tgc ggc tac aca ttt act gac tat gaa ata cac tgg gtg agg 531  
Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg  
155 160 165

cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa 579  
Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu  
170 175 180 185

29

Thr Gly Gly Thr	Ala Tyr Asn Gln Lys	Phe Lys Asp Lys Ala	Ile Val	
	190	195	200	
act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg				675
Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu	205	210	215	
aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac				723
Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp	220	225	230	
tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct cat				771
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser His	235	240	245	
cat cat cat cat cat tagggcctct ctggccgata ccccgaattt ccccgatcgt				826
His His His His His				
250				
tcaaacattt ggcaataaaag				846
<210> 49				
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<221> CDS				
<222> (19)..(687)				
<223> mature peptide is coded by nucleotides 49 to 687				
<400> 49				
cccggttacc cttctaga ctc gtg aca gtt gtt gat ggt gcc caa tcc cag				51
	Leu Val Thr Val Val Asp Gly Ala Gln Ser Gln			
	1	5	10	
ggt caa ctg cag cag tct ggg gct gag ctg gtg agg cct ggg gct tca				99
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser	15	20	25	
gtg acg ctg tcc tgc aag gct tgc ggc tac aca ttt act gac tat gaa				147
Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu	30	35	40	
ata cac tgg gtg agg cag aca cct gtg cat ggc ctg gaa tgg att gga				195
Ile His Trp Val Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly	45	50	55	
gct att gat cct gaa act ggt ggt act gcc tac aat cag aag ttc aag				243
Ala Ile Asp Pro Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys	60	65	70	75
gac aag gcc ata gtg act gta gac aaa tcc tcc agc aca gcc tac atg				291
Asp Lys Ala Ile Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met	80	85	90	
gag ctc cgc agc ctg aca tct gaa gac tct gcc gtc tat tac tat aca				339
Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr	95	100	105	

aga tgg ttt gag gac tgg ggc caa ggg act ctg gtc act gtc tct gca	387
Arg Trp Phe Glu Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala	
110 115 120	
gcc aaa aca aca ccc cca tca gtc tat cca ctg gcc cct ggg tgt gga	435
Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Cys Gly	
125 130 135	
gat aca act ggt tcc tct gtg act ctg gga tgc ctg gtc aag ggc tac	483
Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr	
140 145 150 155	
ttc cct gag tca gtg act gtg act tgg aac tct gga tcc ctg tcc agc	531
Phe Pro Glu Ser Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser	
160 165 170	
agt gtg cac acc ttc cca gct ctc ctg cag tct gga ctc tac act atg	579
Ser Val His Thr Phe Pro Ala Leu Leu Gln Ser Gly Leu Tyr Thr Met	
175 180 185	
agc agc tca gtg act gtc ccc tcc agc acc tgg cca agt cag acc gtc	627
Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Gln Thr Val	
190 195 200	
acc tgc agc gtt gct cac cca gcc agc agc acc acg gtg gac aaa aaa	675
Thr Cys Ser Val Ala His Pro Ala Ser Ser Thr Thr Val Asp Lys Lys	
205 210 215	
ctt gag ccc agc gcggccgctg caggtcttga tcctttcttg ggacccggca	727
Leu Glu Pro Ser	
220	
agaaccaaaa a	738
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<212> DNA	
<213> mouse	
<400> 50	
gcactaggtc aagcggccgc ttactaacac tcattcctgt tg	42
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<211> 753	
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<222> (67)..(705)	
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Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala	
-20 -15 -10	

gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag	96
Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu	
-5 -1 1 5 10	
ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tgc ggc	144
Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly	
15 20 25	
tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg	192
Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val	
30 35 40	
cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act	240
His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr	
45 50 55	
gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa	288
Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys	
60 65 70	
tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac	336
Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp	
75 80 85 90	
tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg	384
Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly	
95 100 105	
act ctg gtc act gtc tct gca gcc aaa aca aca ccc cca tca gtc tat	432
Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr	
110 115 120	
cca ctg gcc cct ggg tgt gga gat aca act ggt tcc tct gtg act ctg	480
Pro Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu	
125 130 135	
gga tgc ctg gtc aag ggc tac ttc cct gag tca gtg act gtg act tgg	528
Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val Thr Trp	
140 145 150	
aac tct gga tcc ctg tcc agc agt gtg cac acc ttc cca gct ctc ctg	576
Asn Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu	
155 160 165 170	
cag tct gga ctc tac act atg agc agc tca gtg act gtc ccc tcc agc	624
Gln Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser	
175 180 185	
acc tgg acc tgc agc gtt gct cac cca gcc agc agc cca agt cag acc	672
Thr Trp Thr Cys Ser Val Ala His Pro Ala Ser Ser Pro Ser Gln Thr	
190 195 200	
gtc acc acg gtg gac aaa aaa ctt gag ccc agc tagtaatgag cggccgctgc	725
Val Thr Thr Val Asp Lys Lys Leu Glu Pro Ser	
205 210	
agatctgac ctttctggg acccgga	753

<210> 52



<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 2253 to 2271  
of pDAB439

<400> 52  
tgcacgtgtt ctcctttttt 19

<210> 53  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 4256 to 4308  
of pDAB439

<400> 53  
ggtacggcca tattggccga gctcggcctc tctggccgat cccc 44

<210> 54  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 4744 to 4807  
of pDAB439

<400> 54  
gcggccgctt taacgcccgg gcatttaaatt ggcgcgcgcgc gatcgcttgc agatctgcat 60  
ggg 63

<210> 55  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 5417 to 5436  
of pDAB439

<400> 55  
ggggactcta gaggatccag 20

<210> 56  
<211> 24  
<212> PRT  
<213> Zea mays

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